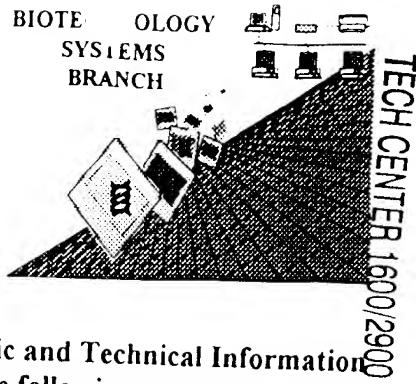


RECEIVED

AUG 31 2001



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 518156

Source: All 1645

Date Processed by STIC: 08/06/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Does Not Comply
Corrected Diskette Needed

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001
TIME: 15:04:53

Input Set : A:\sequence.listing.txt
Output Set: N:\CRF3\08062001\I518156.raw

3 <110> APPLICANT: Tarleton, Rick
4 Garg, Nisha
6 <120> TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC IMMUNIZATION AGAINST INFECTION
AND DISEASE
8 <130> FILE REFERENCE: 235.00201010
10 <140> CURRENT APPLICATION NUMBER: 09/518,156
11 <141> CURRENT FILING DATE: 2000-03-02
13 <150> PRIOR APPLICATION NUMBER: 60/122,532
14 <151> PRIOR FILING DATE: 1999-03-02
16 <160> NUMBER OF SEQ ID NOS: 24
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 8
22 <212> TYPE: PRT
23 <213> ORGANISM: Trypanosoma cruzi
25 <400> SEQUENCE: 1
27 Val Asp Tyr Asn Phe Thr Ile Val
28 1 5
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 8
32 <212> TYPE: PRT
33 <213> ORGANISM: Gallus gallus
35 <400> SEQUENCE: 2
37 Ser Ile Ile Asn Phe Glu Lys Leu
38 1 5
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 34
42 <212> TYPE: DNA
C--> 43 <213> ORGANISM: Artificial
45 <220> FEATURE:
46 <223> OTHER INFORMATION: forward primer
48 <400> SEQUENCE: 3
49 agtcgacgga tccatgattg catttgtcga aggc
52 <210> SEQ ID NO: 4 34
53 <211> LENGTH: 35
54 <212> TYPE: DNA
C--> 55 <213> ORGANISM: Artificial
57 <220> FEATURE:
58 <223> OTHER INFORMATION: reverse primer
60 <400> SEQUENCE: 4
61 atctagaagc ttcatagttc accgacactc agtgg 35
64 <210> SEQ ID NO: 5
65 <211> LENGTH: 35
66 <212> TYPE: DNA
C--> 67 <213> ORGANISM: Artificial
69 <220> FEATURE:
70 <223> OTHER INFORMATION: reverse primer
72 <400> SEQUENCE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001
TIME: 15:04:53

Input Set : A:\sequence.listing.txt
Output Set: N:\CRF3\08062001\I518156.raw

73 atctagaagc ttcatgccgc agcatttgct tc(ccc
76 <210> SEQ ID NO: 6.
77 <211> LENGTH: 0
78 <212> TYPE: PRT
79 <213> ORGANISM: Skipped Sequence)
81 <400> SEQUENCE: 6

35

W--> 82 000
84 <210> SEQ ID NO: 7
85 <211> LENGTH: 8
86 <212> TYPE: PRT
87 <213> ORGANISM: Trypanosoma cruzi
89 <400> SEQUENCE: 7
91 Val Asn His Arg Phe Thr Leu Val
92 1 5
94 <210> SEQ ID NO: 8
95 <211> LENGTH: 8
96 <212> TYPE: PRT
97 <213> ORGANISM: Trypanosoma cruzi
99 <400> SEQUENCE: 8
101 Val Asn His Asp Phe Thr Val Val
102 1 5
104 <210> SEQ ID NO: 9
105 <211> LENGTH: 0
106 <212> TYPE: PRT
107 <213> ORGANISM: Skipped Sequence
109 <400> SEQUENCE: 9

W--> 110 000
112 <210> SEQ ID NO: 10
113 <211> LENGTH: 28
114 <212> TYPE: DNA

28

C--> 115 <213> ORGANISM: Artificial
117 <220> FEATURE:
118 <223> OTHER INFORMATION: forward primer ✓
120 <400> SEQUENCE: 10

121 aggatccatg attgcatttg tcgaaggc
124 <210> SEQ ID NO: 11
125 <211> LENGTH: 30
126 <212> TYPE: DNA

C--> 127 <213> ORGANISM: Artificial
129 <220> FEATURE:
130 <223> OTHER INFORMATION: reverse primer ✓
132 <400> SEQUENCE: 11

30

133 aaagcttcat agttcaccga cactcagtgg
136 <210> SEQ ID NO: 12
137 <211> LENGTH: 26
138 <212> TYPE: DNA

C--> 139 <213> ORGANISM: Artificial
141 <220> FEATURE:
142 <223> OTHER INFORMATION: forward primer

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

errors
when a sequence is skipped
only fields 210 and 400 are
included. (WA)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt
Output Set: N:\CRF3\08062001\I518156.raw

```

144 <400> SEQUENCE: 12
145 aagatcttgt ggaaaggaaat ttgagg
148 <210> SEQ ID NO: 13
149 <211> LENGTH: 28
150 <212> TYPE: DNA
C--> 151 <213> ORGANISM: Artificial
153 <220> FEATURE:
154 <223> OTHER INFORMATION: reverse primer
156 <400> SEQUENCE: 13
157 actcgagtca cagtgggcgg ttgtacag
160 <210> SEQ ID NO: 14
161 <211> LENGTH: 27
162 <212> TYPE: DNA
26
C--> 163 <213> ORGANISM: Artificial
165 <220> FEATURE:
166 <223> OTHER INFORMATION: forward primer
168 <400> SEQUENCE: 14
169 aagatctctg tgaggctgca gacgctg
172 <210> SEQ ID NO: 15
173 <211> LENGTH: 28
174 <212> TYPE: DNA
28
C--> 175 <213> ORGANISM: Artificial
177 <220> FEATURE:
178 <223> OTHER INFORMATION: reverse primer
180 <400> SEQUENCE: 15
181 acccggtta ttggtcgcca ccgtttcc
184 <210> SEQ ID NO: 16
185 <211> LENGTH: 26
186 <212> TYPE: DNA
27
C--> 187 <213> ORGANISM: Artificial
189 <220> FEATURE:
190 <223> OTHER INFORMATION: forward primer
192 <400> SEQUENCE: 16
193 ggttcgattt ggggttgtgt aatata
196 <210> SEQ ID NO: 17
197 <211> LENGTH: 26
198 <212> TYPE: DNA
28
C--> 199 <213> ORGANISM: Artificial
201 <220> FEATURE:
202 <223> OTHER INFORMATION: reverse primer
204 <400> SEQUENCE: 17
205 aaataatgtt cgggkagat gcatga
208 <210> SEQ ID NO: 18
209 <211> LENGTH: 0
210 <212> TYPE: DNA
211 <213> ORGANISM: Skipped Sequence
213 <400> SEQUENCE: 18
26
W--> 214 000
216 <210> SEQ ID NO: 19

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001
TIME: 15:04:53Input Set : A:\sequence.listing.txt
Output Set: N:\CRF3\08062001\I518156.raw

217 <211> LENGTH: 0
 218 <212> TYPE: DNA
 219 <213> ORGANISM: Skipped Sequence
 221 <400> SEQUENCE: 19
 W--> 222 000
 224 <210> SEQ ID NO: 20
 225 <211> LENGTH: 1656
 226 <212> TYPE: DNA
 227 <213> ORGANISM: Trypanosoma cruzi
 229 <400> SEQUENCE: 20
 230 atgcggaaga aagccgcagc attagcagcg cccacagcag acacacggcc gacgtgccgc 60
 232 ggggctgcca ttgccaataa atttatggaa cgtgcccggcc cccgtgaggg cgttgggaga 120
 234 tcaacggaga tgccggctgc tggaccgcg ggtctcaaa gaactcaaac gcaacggggag 180
 236 gtgaaagcgt cacaagacgc cgacgcggcg gccattagta gttatttcca gtcgaattt 240
 238 gtgacatctc agtgcacga gggtgtgtct cctctggcaa agactagggc caacgaacgg 300
 240 cggAACGGGG agcaggagcg ggagaaggaa ctgcccggcgg ttgggtggcgc cgttccaact 360
 242 gggAAAGGGGA cggaccccaa acagcgaatgt ctgcaggatt tgccagcgat gcacgcggag 420
 244 ggacaaaacc agcacggtag agagggtgac aagggtgttt ccgtgaagat ggactcccct 480
 246 ggtcgcgtac aggtgctgga gcaaatttgc ctacacctgg ctgcatttgcgaa cagacagacta 540
 248 gaattagaac ttatagaaac ggcacgggaa ctgacgatgt acaaggagct tttacctgt 600
 250 gtgcagcggcc agaccggagc ccatgctttg tctcaggagc atcacaaggaa gaatagtgt 660
 252 gctccggccac ttagtgcaga tgagaggcga cgacagatgc tctttacagg gcaacaacaa 720
 254 caacagcaac aagtggaa aatgcacccg ggtttagcg ggtggaaac ggcacgcgg 780
 256 agaatgcgt atggttacga ggagggggag agggacgcgg tttcagatgg tgagggccgt 840
 258 ccacgttgcg caggtcgat gggctcccg aagagattcc tttcaacaca accgcctcga 900
 260 agcagcagga accatcgaa ccctcaacgt gctaaccggaa caaatggca tagtcatgtt 960
 262 cccattcgt ccagacaaaa aagtccacccg acaagaggag ctgctgttaac ttccgtaccg 1020
 264 ttggcggcgt ccgcaaccaa tcggcgaggt cggtccatgc gacaacatac ccgaccccg 1080
 266 ggaccttctt atctttcga acgcctcgac gctgaggatg caattgatgat gctggagacg 1140
 268 ctgaaggcgt ctctcatgtt tcgctgcac cactcgcatc atcgatcaac agaaggagat 1200
 270 gttgtgcggc ccggccggaa gccccggaaa ggcacgcggt ctgttccacc accacccgcca 1260
 272 ccacccggccca tgcacaaaga aagcttgcgg ccgcagttgc tggagcggcc 1320
 274 gcatgcacgc tctcagcacg acacggaaagg aaccatggcg tttctgcgtt gggagatccg 1380
 276 tcaaggggca atcgagttc agaaacagct cgcatagctc atgctccctt ttttgggggg 1440
 278 aagaaatgcg cggccggcct aacccaaactc catttctttt ccccttccag aagggtacg 1500
 280 ccgatgaaaa aagacacgcg attgtcacgt ggtcaaggcg ctggagtagc agcagtagcg 1560
 282 gtggcgggtg acggcagct agaggactg cagaggcggtt actggaaaca gtcccggtcg 1620
 284 atattggagc agttgaaaa catgctggca gctgt 1656
 287 <210> SEQ ID NO: 21
 288 <211> LENGTH: 39
 289 <212> TYPE: DNA

C--> 290 <213> ORGANISM: Artificial

292 <220> FEATURE:
 293 <223> OTHER INFORMATION: pTAT linker
 295 <400> SEQUENCE: 21
 296 tccaccatgg ccggtaccgg tctcgaggatg catgcgggt
 299 <210> SEQ ID NO: 22
 300 <211> LENGTH: 14
 301 <212> TYPE: PRT

39

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

C--> 302 <213> ORGANISM: Artificial
304 <220> FEATURE:
305 <223> OTHER INFORMATION: pTAT linker
307 <400> SEQUENCE: 22
309 Gly Ser Thr Met Ala Gly Thr Gly Leu Glu Val His Ala Val
310 1 5 10

312 <210> SEQ ID NO: 23

313 <211> LENGTH: 41

314 <212> TYPE: DNA

C--> 315 <213> ORGANISM: Artificial
317 <220> FEATURE:
318 <223> OTHER INFORMATION: pTAT-HA linker

320 <400> SEQUENCE: 23

321 ccatgtccgg ctagccatat gacgtcccg actatgctgg c

324 <210> SEQ ID NO: 24

41

325 <211> LENGTH: 13

326 <212> TYPE: PRT

C--> 327 <213> ORGANISM: Artificial
329 <220> FEATURE:

330 <223> OTHER INFORMATION: pTAT-HA linker

332 <400> SEQUENCE: 24

334 Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly

335 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:54

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

L:43 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:55 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:67 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:82 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:110 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:127 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:139 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:151 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:163 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:175 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:187 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:199 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:214 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:222 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:290 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:302 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:315 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:327 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/513,156</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	